Table 5. Results obtained by AMINE for the four "unknown" amines.

	Cond DELTA	itions Tallies		
Amine (prefix only)	(ppm)	used?	Solutions (prefix only)	Rank
N-(3-methylbutyl)-1,5-dimethylhexyl	1.5	no	N-(3-methylbutyl)-1,5-dimethylhexyl	-
N-(3-methylbutyl)-2-ethylhexyl	1.5	no	N-(3-methylbutyl)-2-ethylhexyl	-
N-heptyl-N-(3-methylbutyl)-2-ethylhexyl	1.5	yes	N-heptyl-N-(3-methylbutyl)-2-ethylhexyl	1 (tied)
			N-pentyl-N-(3-methylbutyl)-2-ethylhexyl	`1 (tied)
N-pentyl-N-(3,3-dimethylbutyl)- 3,5,5-trimethylhexyl	2.25 ^a	yes	2-ethyl-1,5,5,7,7-pentamethyl-1- (2,2-dimethylpropyl)octyl	1
			N-pentyl-N-(3,3-dimethylbutyl)- 3,5,5-trimethylhexyl	2 (tied)
			N,N-di(<u>tert</u> -butyl)-2-methyl-2- (2,2-dimethylpropyl)hexyl	2 (tied)
			N- <u>tert</u> -butyl-1,1,3-trimethyl-3- (2,2-dimethylpropyl)octyl	2 (tied)
			2-ethyl-1,1,5,7,7-pentamethyl-5- (2,2-dimethylpropyl)octyl	2 (tied)

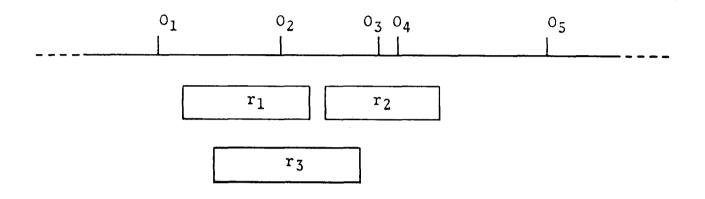
a) With DELTA = 1.5 ppm, no structrures were found for this amine.

Figure captions

- Figure 1. A schematic illustration of R, the alkyl chain-end to be tested by the PRUNER. The group X contains the Nitrogen atom, along with any carbons and hydrogens not included in R.
- Figure 2. The hierarchy of pre-tests used by the PRUNER. A "?" attached to an atom indicates that the neighbors of that atom are unknown at testing time.
- Figure 3. A case in which \underline{r} and \underline{o} do not match when $\underline{n} = N_c$, even though the simple test is passed.
- Figure 4. Sample output from program AMINE (PDP-10 version). The solution structure is written in polish-prefix notation as described in Reference 3a.

$$\begin{array}{c} X = C-? & \longrightarrow CH_2-C-? & \longrightarrow Class \ 1 \ tests \\ & \longrightarrow CH_2-N-? & \longrightarrow Class \ 2, \ 3 \ and \ 4 \ tests \\ & \longrightarrow CH_2-N-? & \longrightarrow Class \ 5 \ tests \\ & \longrightarrow CH & \longrightarrow C-? & \longrightarrow Class \ 5 \ tests \\ & \longrightarrow CH & \longrightarrow C-? & \longrightarrow Class \ 6 \ tests \\ & \longrightarrow CH & \longrightarrow C-? & \longrightarrow Class \ 7 \ tests \\ & \longrightarrow C-? & \longrightarrow Class \ 9 \ tests \\ & \longrightarrow C-? & \longrightarrow Class \ 9 \ tests \\ & \longrightarrow C-? & \longrightarrow Class \ 9 \ tests \\ & \longrightarrow C-? & \longrightarrow Class \ 10 \ tests \\ & \longrightarrow C-? & \longrightarrow Class \ 11 \ tests \\ & \longrightarrow C-? & \longrightarrow Class \ 12 \ tests \\ & \longrightarrow NH_2 \ (Class \ 13 \ test) \\ & \longrightarrow NH_2 \ (Class \ 13 \ tests \\ & \longrightarrow NH_2 \ (Class \ 14 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2 \ (Class \ 15 \ tests \\ & \longrightarrow NH_2$$

Figure 3.



CASE TITLE: N-ETYLYDIPENTYLAMINE
THE AMINE HAS 12 CARBONS
GOODNESS-OF-FIT CRITERION IS 1.500
STANDARD IS TMS
INPUT SHIFTS: 54.00 27.80 30.10 23.00 14.30 47.8

SOLUTION STRUCTURES:

N...C.C.C.C.C.C.C.C.C.C.C SHIFTS: 54.299 27.881 30.239 22.960 14.210 54.29 27.881 30.239 22.960 14.210 47.667 12.86 DELMIN = 0.37

CASE FINISHED. PROCESSING TIME (IN SEC.) WAS 9.711

SIGNIFICANCE

SIGNIFICANCE

Because of the interdisciplinary character of this research, it has a significant impact in medicine, organic chemistry, and computer science. GC/MS has become one of the most powerful techniques available to the organic and biochemist. The potential applications of these techniques in medical research and in the clinic have just begun to be explored. These techniques are of unique importance to medical science since they alone of the current physical methods have sufficient sensitivity and analytical precision to study human biochemistry at the molecular level. Computer automation of these techniques, both at the instrumentation and interpretive levels, would permit the rapid, exhaustive analysis of body fluids across large populations of individuals in various medical contexts and may provide new discoveries important to public health.

In our study of errors of metabolism, accurate diagnosis of the accumulated metabolite provides insight into the biochemical pathogenesis and into therapeutic approaches to the control of such errors. In the case of inherited errors, accurate diagnosis allows reference to published data on the mode of inheritance and, thus, expresses the recurrence risk for genetic counseling purposes. The GC/MS system, with its potential for identification of any metabolites, provides the diagnostic accuracy necessary for a clinical program. GC/MS also provides the methodology for detecting previously unrecognized metabolic errors.

From the point of view of computer science, mass spectrometry is an advantageous environment in which to investigate the concepts necessary for the emulation of lower-level cognitive and manipulative functions as well as for the study of various forms of knowledge representation and automatic theory formation. These concepts will be common in some form to all "intelligent" systems and must be more fully developed from their present primitive state. Mass spectrometry is ideal as a milieu for this research in that it has tremendous practical importance to medicine, is sufficiently complex to challenge the human intellect, and is structured to an extent amenable to computer program formulation within the current state-of-the-art.

COLLABORATIVE ARRANGEMENTS

COLLABORATIVE ARRANGEMENTS

This project is an interdisciplinary research effort involving day-to-day collaboration between Professor J. Lederberg (Department of Genetics), Professor C. Djerassi (Department of Chemistry), Professor E. Feigenbaum (Department of Computer Science), Professor H. Cann (Department of Pediatrics), Dr. B. Buchanan (Computer Science), Dr. A. Duffield (Genetics), Dr. D. Smith (Chemistry), Dr. N. Sridharan (Computer Science), Dr. S. Hammerum (Chemistry), and the Instrumentation Research Laboratory of the Department of Genetics. We are also soliciting additional participation of clinical research interests of the Departments of Medicine and Psychiatry as well as other members of the Department of Genetics (Professors Cavalli-Sforza and Herzenberg). The proximity of these people and facilities in a medical environment offers a highly unique opportunity for collaborative interaction.

FACILITIES AVAILABLE

FACILITIES AVAILABLE

We will derive much of the clinically significant material for analysis from patients in the Premature Research Center and the Clinical Research Center of the Department of Pediatrics at Stanford. Analyses will be performed on existing gas chromatograph and mass spectrometer instrumentation. We have available a GC-coupled Finnigan 1015 quadrupole instrument in the Department of Genetics and a GC-coupled Varian-MAT 711 instrument in the Department of Chemistry. Also available in the Department of Chemistry are MS-9 and Varian-MAT Ch-4 instruments.

We will derive our computing resources from existing PDP-11/20 mini-computer systems which interface the mass spectrometer instruments as well as from the ACME follow-on 370/158 computer at Stanford for data reduction and graphics support. Artificial intelligence program development will be carried out on the Stanford Computation Center IBM 360/67 and machines available over the ARPA computer network. GC/MS data will be interfaced to these programs through standard communication links.

HUMAN SUBJECTS

As a part of this research project, GC/MS analysis techniques will be applied to human body fluids in collaboration with clinical investigators and blood and urine specimens will be collected from human subjects. Collection of VOIDED URINE SPECIMENS presents no risk to the patient. Collection of 5-10 ml of blood by venepuncture is a procedure attended by minimal risk; infection is a remote possibility, especially from deep venepuncture (e.g. femoral tap). However, superficial veins are usually used in children, and even infants. It is only the occasional infant that requires a femoral tap and this procedure would be deferred for this project unless the specimen was essential for diagnosis.

BUDGETS AND JUSTIFICATION

In the following budget estimates, the abbreviations listed below are used to denote departmental affiliation or professional specialty:

G - Genetics

CS - Computer Science

Ch - Chemistry

E - Electrical Engineering

BUDGET - PART A

APPLICATIONS OF ARTIFICIAL INTELLIGENCE TO MASS SPECTROMETRY

Subtotal - Trainee Expenses

11.

c. TRAINEE TRAVEL (Describe)

12. TOTAL DIRECT COST (Add Subtotals, Items 9 and 11, and enter on Page 1)

\$ 123,574

BUDG	ET ESTIMAT	ES FOR ALL		UPPORT REQ		M PUBLIC H	EALTH SERV	ICE
		1ST PERIOD (SAME AS DE-	ADDITIONAL	YEARS SUPPO	RT REQUESTE	D (This applicat	ion only)	
DESCRIPTION		TAILED BUDGETI	2ND YEAR	3RD YEAR	4TH YEAR	5TH YEAR	6TH YEAR	7TH YEAR
PERSONNEL COSTS		80,624	95,175	100,320				
CONSULTANT (Include fees, tra		1,100	1,200	1,300				
EQUIPMENT		_		-				
SUPPLIES		350	400	450				
	DOMESTIC	1,400	1,600	1,800				
TRAVEL	FOREIGN							
PATIENT COSTS		_	_	-				
ALTERATIONS AND RENOVATIONS		_	_	-				
OTHER EXPENSES		40,100	45,450	50,000				
TOTAL DIRECT COSTS 123		123,574	143,825	153,870		,		
TOTAL FOR E	NTIRE PROPO	SED PROJECT P	PERIOD (Enter o	on Page 1, Item 4	1) ———	\$ 421,	269	

REMARKS: Justify all costs for the first year for which the need may not be obvious. For future years, justify equipment costs, as well as any significant increases in any other category. If a recurring annual increase in personnel costs is requested, give percentage. (Use continuation page if needed.)

See attached budget justification notes.

BUDGET - PARTS B (i) AND B (ii)

MASS SPECTROMETER DATA SYSTEM DEVELOPMENT

AND

ANALYSIS OF THE CHEMICAL CONSTITUENTS OF BODY FLUIDS

ONLY

b. TUITION AND FEES

c. TRAINEE TRAVEL (Describe)

12. TOTAL DIRECT COST (Add Subtotals, Items 9 and 11, and enter on Page 1)

Subtotal - Trainee Expenses

\$

^{\$} 237,530

BUDGET ESTIMATES FOR ALL YEARS OF SUPPORT REQUESTED FROM PUBLIC HEALTH SERVICE **DIRECT COSTS ONLY (Omit Cents)** 1ST PERIOD (SAME AS DE-TAILED BUDGET) ADDITIONAL YEARS SUPPORT REQUESTED (This application only) DESCRIPTION 2ND YEAR 3RD YEAR 4TH YEAR 5TH YEAR 6TH YEAR 7TH YEAR **PERSONNEL** 139,830 148,066 156,775 COSTS **CONSULTANT COSTS** (Include fees, travel, etc.) **EQUIPMENT** 3,000 3,000 3,000 20,400 21,050 22,250 SUPPLIES 1,000 DOMESTIC 1,000 1,000 TRAVEL **FOREIGN** PATIENT COSTS ALTERATIONS AND 2,500 RENOVATIONS OTHER EXPENSES 70,800 75,000 79,500 TOTAL DIRECT COSTS 237,530 248,116 262,525 \$ 748,171 TOTAL FOR ENTIRE PROPOSED PROJECT PERIOD (Enter on Page 1, Item 4) -

REMARKS: Justify all costs for the first year for which the need may not be obvious. For future years, justify equipment costs, as well as any significant increases in any other category. If a recurring annual increase in personnel costs is requested, give percentage. (Use continuation page if needed.)

See attached budget justification.

BUDGET - PART C

EXTENSION OF THE THEORY OF

MASS SPECTROMETRY BY COMPUTER

DESCRIPTION		1ST PERIOD (SAME AS DE TAILED BUDGET)	ADDITIONAL YEARS SUPPORT REQUESTED (This application only)						
			2ND YEAR	3RD YEAR	4TH YEAR	5TH YEAR	6TH YEAR	7TH YEAR	
PERSONNEL COSTS		48,521	61,194	64,655					
CONSULTAN		-	_	_					
EQUIPMENT		-	_	_					
SUPPLIES		350	400	450					
TRAVEL -	DOMESTIC	1,400	1,600	1,800					
	FOREIGN								
PATIENT COSTS		_	-	_					
ALTERATIONS AND RENOVATIONS		-	-	_					
OTHER EXPENSES 23		23,500	27,650	30,450					
TOTAL DIRECT COSTS 73,771		90,844	97,355		•				

REMARKS: Justify all costs for the first year for which the need may not be obvious. For future years, justify equipment costs, as well as any significant increases in any other category. If a recurring annual increase in personnel costs is requested, give percentage, (Use continuation page if needed.)

See attached budget justification notes.